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**ARABIDOPSIS THALIANA FAE1 PROMOTER:
(LENGTH 934 bp)**

-950 ACTCA TAAAAAACTAG TAGATTGGTT GGTGGGTTTC CATGTACCG

AtproFW →

-900 AAGGCCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCCC TACTCAATTC

-850 CTAGTTGTGT AAATGTATGT ATATGTAATG CGTATAAAAC GTAGTACTTA

-800 AATGACTAGG AGTGGTTCCT GAGACCGATG AGAGATGGGA GCAGAACTAA

-750 AGATGATGAC ATAATTAAGA ACGAATTTGA AAGGCTCTTA GGTTTGAATC

-700 CTATTCGAGA ATGTTTTTGT CAAAGATAGT GGCGATTTTG AACCAAAGAA

-650 AACATTTAAA AAATCAGTAT CCGGTTACGT TCATGCAAAT AGAAAGTGGT

-600 CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCAATC

-550 CTGGCTGTGT ACAAACTAC AAATAATATA TTTTAGACTA TTTGGCCTTA

-500 ACTAAACTTC CACTCATTAT TTACTGAGGT TAGAGAATAG ACTTGCGAAT

-450 AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGTAT

-400 GCCAATCAGA TCTAAGAACA CACATTCCCT CAAATTTTAA TGCACATGTA

-350 ATCATAGTTT AGCACAAATC AAAAATAATG TAGTATTTAA GACAGAAATT

-300 TGTAGACTTT TTTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT

-250 TATTTTAAGT GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA

-200 TATATATTTT TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTCAGTGGA

-150 CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT

-100 GTCTAAATGC ATGCTTTGCA AAACGTAACG GACCACAAAA GAGGATCCAT

-50 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA

← AtproRV

1 [ATG]ACGTCCG TTAACGTTAA GCTCCTT

FIG. 1

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FIG. 2A

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**BRASSICA NAPUS FAE1 PROMOTER:
(CONTINUED)**

-450 GTTACATAGA TTTGGAAACA CTTCATCTAG CTCAATATGG TATGAGTTGG
-400 CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG
-350 ATTGCTTTAG GGT CAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT
-300 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA
-250 GATACCCGGT CAAAATTGAT TCTGATTCAG GTAAGTCAGA GACTCGTGTC
-200 CAAAACGGTC GGTCCTAATA AACGATGTTT GCTCTCTTTC GTTTCTTTTT
-150 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
-100 TAAAGAATGC AATGGTGTTT TAGTATTTGA TTGTTTTACA TGTATGTATC
-50 TCTTATTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCGG
1 ATGACGTCCA TTAACGTAA GCTCCTTAC CATTCAGTCA TAACCAACCT
51 TTTCAACCTT TGCTTCTTTC CGTTAACGGC GATCGTCGCC GGAAAAGCCT
101 ATCGGCTTAC CATAGACGAT CTTCACTACT TATACTATTC CTATCTCCAA
151 CACAACCTCA TAACCATCGC TCCACTCTTT GCCTTCACCG
← **BnproRV**
← **Bnwalk2**
← **Bnwalk1**

FIG. 2B



4/15

LUNARIA ANNUA FAE1 PROMOTER:
(LENGTH 1069 bp)

-1100 CG CCGGGGAGTT TCAGCTTAAC CGGTAAAATT
LaproFW →
-1050 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTGT
-1000 TGTTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATAAA
-950 GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
-900 TGGCCTCTTA GGTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
-850 GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC
-800 TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
-750 AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
-700 AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
-650 ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
-600 TTTTATTTGG CACAACTTG TTTTACTTTT CTACCTTATA ATTTGGAAC
-550 TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
-500 AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
-450 CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
-400 TCGGATCAGT ATTCTTAAAT AAGAATATAA AACTAATTCA ATAGTTACAG
-350 ATAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
-300 TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTTTATA
-250 TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
-200 TATTAATTAA TATTTTTTTT ATCGGACTAC TTTCTATTT TGGCACCTTT
-150 CATCTGACTA CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA

FIG. 3A

**LUNARIA ANNUA FAE1 PROMOTER:
(CONTINUED)**

```

-100 ATACACATGT CTATATAAAT GCATGTAAAA CGTAACGGAC CACAAAAGTG
-50 GATCCATACA AATACATCTC ATCGCACCCT CTCCGACACA AAACTGAACA
                                     ← LaproRV
  1  ATGACGTCTG TGAACGTAA ACTCCTTTAC CATTACGTCA TAACCAACTT
51  TTTCAACCTC TGTTTCTTCC CACTGACGGG GATCCTCGCC GGAAAAGGCT
                                     ← Lawalk2
101  CTCGTCTTAC CACAAACGAT CTCCACCA
                                     ← Lawalk1

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FIG. 3B

ALIGNMENT OF *A.t.*, *L.a.* AND *B.n.* *FAE1* PROMOTERS

CLUSTAL W (1.74) MULTIPLE SEQUENCE ALIGNMENT

FIG. 4A

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7/15

ALIGNMENT OF *A.t.*, *L.a.* AND *B.n.* *FAE1* PROMOTERS (CONTINUED)

A.t. TTGGTTTCCA--TGTACCAGAAGGCTTACCCTAT-TAGTTGAAAGTTGAACTTTGTTC
L.a. TTGTTACTCAATTGGGCTAAGTGTATTATTATAT-GTGTGTATATAATAAAGGTAGAAC
B.n. ACTTGTTCATGTCCATAAAATACGTATGCTCTTGTGGTGAGCACAGAGAACATCACTT
 ** * * * *
 Con. 4 WYKKKWYBCANNTSBRYHARRWKDMKTAYBMTMTNKWGKTGWRHRYWRWRAMBDTVDHYY

A.t. CTAATCAATTCCTAGTTGTGTAAATGT---ATGTATATGTAAT---GCGTATAAAACGTA
L.a. GTAA--ATTTACTAAGAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTG
B.n. ATAA-CATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTCCTGTT
 ** * * * *
 Con. 4 VTAMNNAWTTMCMMDKDDKRTRWWKKNNNATGWDDDTKYHMWNNGCBTVTWMVRYKTD

A.t. GTACTTAAATGACTAGGAGTGGTCTTGAGACCGATGAGAGATGGGAG-CAGAACTAAG
L.a. AATCCTACTCGAGAAG-ACTAATTTTAAATTTACTGGCAAAAATAGAAA-TCAATTTATAA
B.n. GGTGGGGC-CGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGACGGTCCAAGTACGA
 * * * * *
 Con. 4 RDWSBKRMNYGMBWKNWSYDVTTYWVWDDMCKRKVRRWVRTRGRMRNYMVAWBTAHRR

A.t. AT--GATGACATAATTA-----AGAACGAATTTGA-AAGG-CTCTTAGGTTTGAATCCT
L.a. GT--GTTTAAACAAATCGATGGTATACTGATTAGT-GATCACTCTTAGGTTTGTATCCA
B.n. GCTAGTTTCACACGGTTTCAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCA
 * * * * *
 Con. 4 RYNNGWTBAMAYRRWTMNNNNNNNAKAMCKRAKYWGWNRABVNSTCTTWKSKTTKVRTSCW

A.t. ATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAAAGAAAACATTTAAA-A
L.a. ACTCGAGTATTGAGTATTGAACGCTT-----TTTTTAAATAAAATCTTGATTTTTTA-A
B.n. A--CAAGGA-GACGATGAGAACGGCAA-----AATCGGAGTGAGTTTGTCCAAGGACATA
 * * * * *
 Con. 4 ANNCRAGDANKDHKWKWSAAMGVYWNNNNNNNNTYKKAHBRWDWVHSAWKKWHANA

A.t. AATCAGTATCCGGTTAC----GTTTCATGCAAATAGAAAGTGGTCTA---GGATCTGATT-
L.a. ATTGGTTTTTTGAGTAAAAAAGTTCTTAATATTTCTCTTTGTTTTAATGGGTTTGTTT-
B.n. ACCGATGTTGCTGGTCAACGGTTAAGAAAAACATAGCAACGTT-----GGGTCCGTTGA
 * * * * *
 Con. 4 AHYSRKKWTBYKRKTMVNNNNNGTTMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKN

A.t. GTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGCT-GTGTACAAAAC
L.a. TGCATTTTATAAGCTTAATTTTTCTAATTTAATATTTTATCTATCATCGTCCGTAAAGTT
B.n. TTCTTCCGTTAAGCGAGAAACTTCTT--TTTTTCGTTA--CCTTCATGGGCAAGAAACTT
 * * * * *
 Con. 4 KKMWTYYKWKANNCCKWRAWDHKTCTHNNTTWWMKTYWNNCYWKSMTNGKSHRBAAAVYT

A.t. ACAATAATATA----TTTAGACTATTTGGCCTTAACTAACTTCCA-CTCATTATTTA
L.a. TTATTTGGCACAACTTGTTTTACTTTTCTACCTTA--TAATTTGGGAAGTGGTGGAGT-
B.n. TTCAAAGATAAAATCAACATTACTACGTCCCGGATTTCAAACCTTGCTATTGACCATTTT
 * * * * *
 Con. 4 WYMWWRRYAHANNNNWDYWWKACTWYKYBVCCKWNNYAAYWTKSSWNYTSRYRWKTN

A.t. -CTGAGGTTAGAGAA--TAGACTTGCGAATAAACACATTCCCGAGAAATACTCATGATCC
L.a. -CAAAGCGTACCGGA--CAAATATGTTT-TATATTCTTATTTAAGAATTAACACTCATCT
B.n. TGTATACATGCCGGAGGCAGAGCCGTGATTGATGTCTAGAGAAGAACCAGCCCTAGCA
 * * * * *
 Con. 4 NSWRWRS DTRSMGRANNYARABHYGYKWNTRWWBWSHTWBHBRAGAAHYWMBMMYBAKCH

FIG. 4B



8/15

ALIGNMENT OF *A.t.*, *L.a.* AND *B.n.* *FAE1* PROMOTERS (CONTINUED)

CE3

A.t. CATAATTAGTCAGAGGGTATG-----CCAATCAGATCTAAGAAACACATTCCCTC
L.a. CATAATTAGTCAGAGGCTAGGGAGATTAGCCAATCAATGCTAACACAAA-ATTCTCTT
B.n. CCGATCGATGTAGAGGC-----ATCAAGATCAACGTTACATAGATTGG

* *

Con. 4 CMKAWYKAKKYAGAGGSNNNNNNNNNNNNNNNNNNNNATCARDYYAASRWYAMANAKWYYYKB

A.t. AA--ATTTTA--ATGCAC-ATGTAATCAT-----AGTTT-----AGCACAAATTCAAAA
L.a. AATGATCTAACGATGCT--ATTTAATATTCCGGATCAGTATTCTTAAATAAGAATATAAAA
B.n. AAACACTTCATCTAGCTCAATATGGTATG-----AGTTGGCATACAT-AGAAG-CAAAA

* *

Con. 4 AANNAYYTHANNWGCWNNATDTRRTMWKNNNNNNNAGTWKNNNNNNNAKNASAAKNYAAAA

A.t. ATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT---TTGGCGT-TAAAGG
L.a. CTAATTCATAGTTACAGATAAAAACCTTATATAGACTTTTTTAT--TTGGAATATAAAAG
B.n. GGAAGGATGAA-GAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTTAAGTG

* *

Con. 4 VKAAKKHWRWANKWAMRGWHADAAABTTDKRNNGAYTKYTTNNNNNTYRGVVTNTAARDG

A.t. AA-----GACTAAGTTTATA-CGT-----ACATTT-TATTTTAAGT
L.a. TATCAATATATTATA-GACAATATTTATAACGTTAAAAATACAATATTTTATTTTAT
B.n. TAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCTCTGGGA

* *

Con. 4 WANNNNNNNNNNNNNGWSDMWVTWVAYANYGTNNNNNNNNNNAYAWWTNKWYYTTDDRW

CE1

A.t. GGA-----AAACCGAAATT--TCCATCGAAATATATGA--ATTT-AGTATAT---
L.a. ATATTTATTTCAAATTGAAAGCATTACTTCTATCGAAATGA--ATTTTAGTATATTAAT
B.n. ACACT-----GCATCGACAGATACCCGGTCAAATGATTCTGATTCTAGGTAAGTCAGA

* *

Con. 4 RBAYTNNNNNNRMAYYGAYADDYAYYMSDTCDAWMKWDAKMNNTTYNRGTAWRTNNNN

G-box2

A.t. --ATATTTCTGCAAT-----GTACTATTTTGCTATTTTGGCAA-CTTTCAGTGGACTAC
L.a. TAATATTTTAAATC-----GGACTACTTTCTATTTTGGCAC-CTTTCATCTGACTAC
B.n. GACTCGTGTCACAAACGGTCCGTCTAATAAACGATGTTTGCTCTCTTTCTTTCTTT

* *

Con. 4 NNMTMKTKYBHAAWNNNNNNGKMCTAHTWWVCKATKTTKGCWMNCTTTCRKYKNNCTWY

G-box1

A.t. TACTTTATTACAATGTGT--ATGGATGC-ATGAG---TTTGAGTA-TACACATGCTATAA
L.a. TAATTTATTTCAATGTGT--ATGCATGC-ATGAG---CATGAGTAATACACATGCTATA
B.n. TTATTTGTTATAATAATTTGATGGCTACGATGTTTCTCTGTTTGTATGAATAAAGAAT

* *

Con. 4 TWMTTTRTTWYAATRWKTNNATGSMTRCNATGWKNNNYWTGWKTRWTAYRMATRWKAWW

A-300 EM1 ABA

A.t. TGCATGCT-TTGCAAAACGTAACGGACC-ACAAAAGAGGATCCAATGCAAAATACATCTCAT
L.a. TAAATGCA-T-GTAAAACGTAACGGACC-ACAAAAGTGGATCCATACAAATACATCTCAT
B.n. GCAATGGTGTCTAGTATTTGATTGTTTTACATGTATGTATCTCTT-ATTTACATGAAAT

* *

Con. 4 KVMATGSWNTNSYARWAYKTRAYKGWYNNACAWRWRWGKATCYMTDNAWWTACATSWMAT

A.t. AGC-TTCCTCCATTATTTTCCGACACAAA-CAGAGCA---
L.a. CGC-ACCCTC-----TCCGACACAAAACCTGAACA---
B.n. TTTTAAACGCC-----TAAAAAAGGGAATCCG

* *

Con. 4 HKYNWHMCKCNNNNNNNNNTMMRAMAMAAANCDGARYWNNN

FIG. 4C



9/15

ALIGNMENT OF *A.t.* AND *L.a.* *FAE1* PROMOTERS
 CLUSTAL W (1.74) MULTIPLE SEQUENCE ALIGNMENT

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A.t. -----ACTCATAA
L.a. CGCCGGGGAGTTTCAGCTTAACCGGTAAATTTGGCCTGTACATATATTTACCACTGAGTA
Con.5 ACTSAKWA

A.t. AAACTAGTAGAT--TGGTTGGTTGGTTTCCA--TGTACCAGAAGGCTTACCCTATTAGTT
L.a. AAGACATCAGTTAATGATTTGTTGTTACTCAATTGGGCTAAGTGATATTATATATGTGTT
Con.5 AARMYAKYAGWTNNTGRTTKGTTGKTWYYCANNTGKRCYARRWGKMTTAYYMTATKWGTT

A.t. GAAAGTTGAAACTTTGTTCCCTACTCAATTCCTAGTTGTGTAAATGT---ATGTATATGT
L.a. GTATATAATAAAGGTAGAACGTAA--ATTACTAAGAATGTGTTTTTCCAATGTGATTGC
Con.5 GWAWRTWRWAAMKKTRKWMCMSTAMNNAWTTMCTARKWRTGTRWWTKTNNNATGTRWWTGY

A.t. AAT---GCGTATAAAACGTAGTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGA
L.a. TCTTTGGCCTCTTAGGTTTGAATCCTACTCGAGAAG-ACTAATTTTAATTTACTGGCAA
Con.5 WMTNNNGCSTMTWARRYKTRRWWCYTAMWYGASWAGNASTRTTYTWRWKWCKRKSARA

A.t. GATGGGAGCAGAACTAAAGATGATGACATAATTA-----AGAACGAATTTGAAAGG-CT
L.a. AATAGAAATCAATTTATAAGTGTTTAAACAAATCGATGGTATAACTGATTAGTGATCACT
Con.5 RATRGRARYMRAWYTAWARRTGWTAMAYAAWTMNNNNNNAKAACKRATTWGWRAKSNT

A.t. CTTAGGTTTGAATCCTATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAA
L.a. CTTAGGTTTGTATCCAACCTCGAGTATTGAGTATTGAACGCTT-----TTTTTAAATAA
Con.5 CTTAGGTTTKRATCCWAYTCGAGWATKKWKTWKTSAAMGMTWNNNNNNNTTTTKAAMYAA

A.t. AGAAAACATTTAAAAATCAGTATCCGGTTAC---GTTTCATGCAAATAGAAAGTGGTCT
L.a. AATCTTGATTTTAAATTTGGTTTGTGAGTAAAAAAGTTCTTAATATTTCTCTTTGTTT
Con.5 ARWMWSATTTWAAAWTSRKWTYTYGRKTAMNNNNGTTCTWTRMWAWTWKWMKTKGTTT

A.t. A---GGATCTGATTGTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGC
L.a. TAATGGGTTTGTGTTTGCATTTTATAAGCTTAATTTCTTAATTTAATATTTATCTATCA
Con.5 WNNNGGRITYTGWTTKKMATTTTAKANNCTTAAWKWKCTMNNNTTAAKATTYWATCYWKSM

A.t. T-GTGTAACAACTACAAATAATATA----TTTAGACTATTTGGCCTTAACCTAACTTC
L.a. TCGTCCGTAAAGTTTATTTGGCACAACTTGTTTTACTTTTCTACCTTA--TAATTTGG
Con.5 TNGTSYRYAAARYTWYAWWTRRYAYANNNTKTWKACTIONTYYKRCCTANNTAAWYTKS

A.t. CA-CTCATTATTTACTGAGGTTAGAGAATAGACTTGCGAATAAACACATTCCCGAGAAAT
L.a. GAACTGGTTGAGT-CAAAGCGTACGGGACAAATATGTTT-TATATTCTTATTTAAGAATT
Con.5 SANCTSRTRWKTNCWRAGSKTASMGRAAYARAYWTGYKWNTAWAYWCWTWYYYRAGAAWT

A.t. -432 ACTCATGATCCCATAATTAGTCAGAGGGTATG-----CAATCAGATCTAAGAACA
L.a. AACACTCATCTCATAATTAGTCAGAGGGCTAGGGAGATTGAGCCAATCAATGCTAACAACA
Con.5 AMYMTSATCYCATAATTAGTCAGAGGSTAKGNNNNNNNNNCCAATCARWKCTAASAACA
  
```

FIG. 5A



10/15

ALIGNMENT OF *A.t.* AND *L.a.* *FAE1* PROMOTERS (CONTINUED)

<i>A.t.</i>	-381	CACATTCCCTCAA--ATTTTA--ATGCACATGTAATCAT-----AGTTT-----AGCA
<i>L.a.</i>		AA-ATTCTCTTAATGATCTAACGATGCT-ATTTAATATTCGGATCAGTATCTTAAATAA * * * * *
<i>Con.5</i>		MANATTCTCYCTYAANNATYTWANNATGCWNATKTAATMWTNNNNNNAGTWTNNNNNNNAKMA
<i>A.t.</i>	-337	CAATTCAAAAATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT--TTGGCG
<i>L.a.</i>		GAATATAAACTAATTCAATAGTTACAGATAAAACTTATATAGACTTTTTTATTTGGAA * * * * *
<i>Con.5</i>		SAATWYAAAAMTAATKYARTANTTAMAGAYARAAAYTTRTANNGACTTTTTTNNTTGGMR
<i>A.t.</i>	-282	T-TAAAGGAA-----GACTAAGTTTATA-CGT-----ACATTT-TAT
<i>L.a.</i>		TATAAAAGTATCAATATATTATAGACAATATTTATAACGTTAAAAATACAATATTTATAT * * * * *
<i>Con.5</i>		TNTAAARGWANNNNNNNNNNNNNGACWAWRTTATANCGTNNNNNNNNNNAYATTTNTAT
<i>A.t.</i>	-247	TTTAAGTGGA-----AAACCGAAATT--TTCCATCGAAATATATGAATTT-AGTATA
<i>L.a.</i>		TTTTTATATATTTTATTTCAATTGAAAAGCATTACTTCTATCGAAATGAATTTTAGTATA * * * * *
<i>Con.5</i>		TTTWWRTRKANNNNNNNNNNAAAYYGAAWKNNTTMCWTCKAWMKAWATGAATTTNAGTATA
<i>A.t.</i>	-198	T-----ATATTTCTGCAAT-GTACTATTTTGCTATTTTGGCAACTTTTCAGTGGACTACT
<i>L.a.</i>		TTAATTAATATTTTTTTAATCGGACTACTTTCCTATTTTGGCACCTTTCATCTGACTACT * * * * *
<i>Con.5</i>		TNNNNNNATATTTYTKYAATNGKACTAYTTTSCATTTTGGCAMCTTTCACYKGACTACT
<i>A.t.</i>	-145	ACTTTATTACAATGTGTATGGATGCATGAGTTTGAGTA-TACACATGTCTAAATGCATGC
<i>L.a.</i>		AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATACACATGTCTATATAAATGC * * * * *
<i>Con.5</i>		AMTTTATTWCAATGTGTATGSATGCATGAGYWTGAGTANTACACATGTCTAWATRMATGC
<i>A.t.</i>	-86	TTTGCAAAACGTAACGGACCACAAAAGAGGATCCATGCAAATACATCTCATAGCTTCCTC
<i>L.a.</i>		AT-GTAAACGTAACGGACCACAAAAGTGGATCCATACAAATACATCTCATCGCACCTC * * * * *
<i>Con.5</i>		WTNGYAAAACGTAACGGACCACAAAAGNGGATCCATRCAAATACATCTCATMGCWYCCTC
<i>A.t.</i>	-26	CATTATTTTCCGACACAAA-CAGAGCA
<i>L.a.</i>		-----TCCGACACAAAAGTGAACA * * * * *
<i>Con.5</i>		NNNNNNNTCCGACACAAANCWGARCA

FIG. 5B



11/15

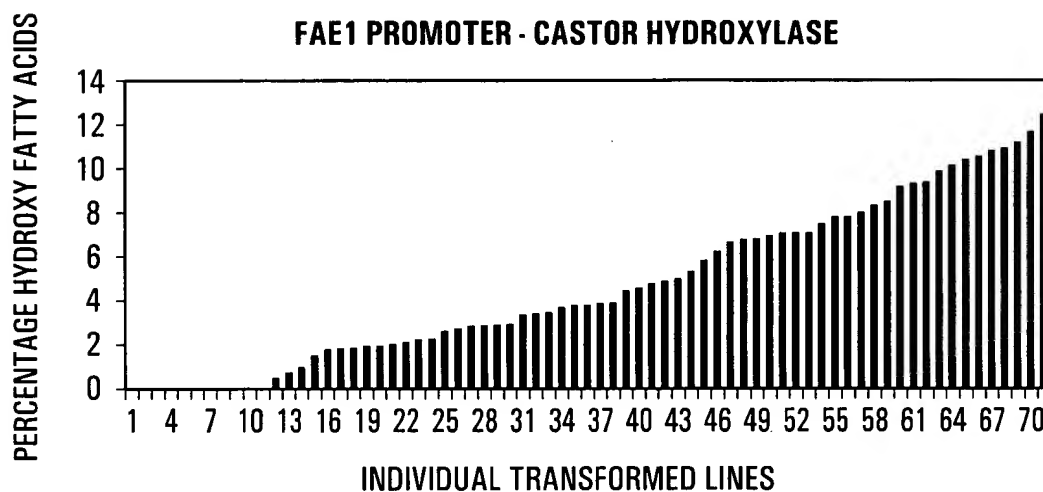


FIG. 6A

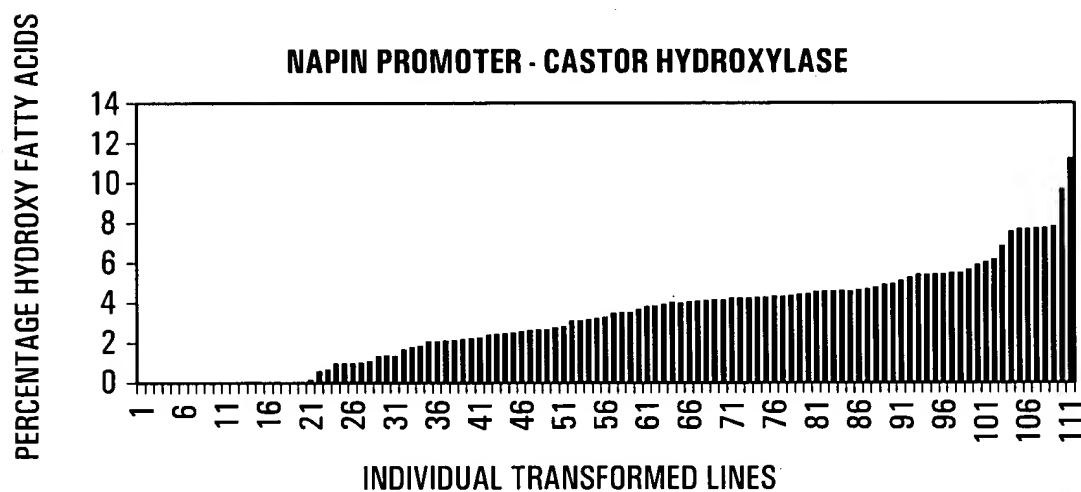


FIG. 6B



12/15

Alignment of B.n. and L.a. FAE1 promoters
 CLUSTAL W (1.81) multiple sequence alignment

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BnFAE1  GGTGGGCAAACTCTGACTTCACCAAGAAACAACCTCGAGTCGTTATCCATCTCCTCATAA 60
LaFAE1  -----

BnFAE1  CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTCTCTACATCGCAACCCGGC 120
LaFAE1  -----

BnFAE1  CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180
LaFAE1  -----CGCCGGGGAGT-TTCAGCTTAACCGGTAAATTGGCCTGTACATATA 46
      * * * * *

BnFAE1  GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
LaFAE1  TTTACCACTGAGT-AAAGACATCAGTTAATGATT-----GTTGTTACTCAATTGGGCT 99
      * * * * *

BnFAE1  GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTTTCAGGTC 300
LaFAE1  AAGTGTATTATTATATGTGTG-----TATATAATAAAGGT---AGAACGT--AAATT 147
      * * * * *

BnFAE1  TAGGCGATGAACTCACGGGGCCGAGGGGCTGCTTCAGGTCCCTCCCCGGAAGACTTTTG 360
LaFAE1  TA--CTAAGAAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTGAATCCTA 205
      * * * * *

BnFAE1  CGCGGGCGCGTGAAGAGACGGAGCAAGTTATCATTGGTGGCTAGAAAATCTATTCAAGA 420
LaFAE1  CT-----CGAGAAGACTAATTTTAAAT-TTACTGGCAAAAATAGAAATCAATTATATA 256
      * * * * *

BnFAE1  ACACCAACGTTAACCCTAAAGATATAGGTATACTTGTGGTGAACCTCAAGCATGTTTAATC 480
LaFAE1  GTGTTTAAACAAATC--GATGGTATAACTG-ATTAGTGATCACTCTTAGGTT--TTGATC 311
      * * * * *

BnFAE1  CAACTCCATCGCTCTCCGCGATGGTTCGTTAACACTTTCAAGCTCCGAAGCAACGTAAGAA 540
LaFAE1  CAACTCGAGTATTG-----AGTATTGAACGCTTT-----TTTTAAATAAATCTTGA 358
      * * * * *

BnFAE1  GCTTTAACCTTGGTGGCATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTAGCAAAGG 600
LaFAE1  TTTTAA--TTGGTTTTTTGAGTAAAAAAGTCTTAATATTTCTCTT-TGTTTTAATGG 416
      * * * * *

BnFAE1  ACTTGTTCATGTCC-ATAAAAATACSTATGCTCTTGTGGTGAGCAGAGAACATCACT 659
LaFAE1  GTTTGTTTTGCATTTTATAAGCTTAATTTTCTAATTTAAT-ATTTATCTATCATCGTC 475
      * * * * *

BnFAE1  TATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTCCTGTT 719
LaFAE1  CGTAAAGTTT-----TATTTGSCACAACTTGTTTTA---CTTTCTACCTTATA 522
      * * * * *

BnFAE1  GTGGGGCCGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGACGGTCCAAGTACGAG 779
LaFAE1  ATTTGGGA-CTGGTTGAGTCA-----AAGCGTACCGGACAAATATGTTTATATTC--- 573
      * * * * *

BnFAE1  CTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCAA 839
LaFAE1  -TTATTTA-AGAATTAACACTCATCTCATAATTAGTCAGAGGC-----TAGGGAGATT 624
      * * * * *

BnFAE1  CAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTSTCCAAGGACATAACCGATGTT 899
LaFAE1  CAGCCAATCAATGCTAACACAAATTTCTTTAA--TGATCTAACGATGCTATTTAATAT 682
      * * * * *
  
```

FIG. 7A



13/15

Alignment of *B.n.* and *L.a.* *FAE1* promoters

BnFAE1	GCTGGTCGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTCCGTTA-AG	958
LaFAE1	TCGGATCAGTATTCTTAAATAAGAATATAAA-----ACTAATTCAATAGTTACAG	732
	* * * * *	
BnFAE1	CGAGAAACTTCTTTTTTCGTTACCTTCATGGGCAAGAAACTTTTCAAAGATAAAATCAA	1018
LaFAE1	ATAAAACTTATATAGACTTTTTTATTTG-GAATATAAAAGTATCAATATATTATAGACA	791
	* * * * *	
BnFAE1	ACATTACTACGTCCCGGATTTCAAACTTGTATTGACCATTTTTGTATACATGCCGGAGG	1078
LaFAE1	ATATTTATA-----ACGTTAAAAATACAATATTTATATTTTTATATATTTTATTCAAA	845
	* * * * *	
BnFAE1	CAGAGCCGTGATTGATGTGCTAGAGAAGAACTAGCCCTAGCACCGATCGATGTAGAGGC	1138
LaFAE1	TTGAAAAGCATTACTTCTATCGAAATGAATTTTAGT----ATATTAATTAATATTTT	901
	* * * * *	
BnFAE1	ATCAAGATCAACGTTACATAGATTGGAACACTTCATCTAGCTCAATATGGTATGAGTT	1198
LaFAE1	AATCGGACTACTTTCTCTAT----TTTGGCACCTTTTCATCTGACT-----ACT	944
	* * * * *	
BnFAE1	GGCATACATAGAAGCAAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTT	1258
LaFAE1	AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATA-----CACATGCTCTAT	996
	* * * * *	
BnFAE1	AGGGTCAGGCTTTAAGTGTACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTC	1318
LaFAE1	ATAAATGCATGTAAAACGTAAACGG-ACCACAAAGTGGATCCATACAAATACATCTCATC	1055
	* * * * *	
BnFAE1	GACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAATTTGATTCTGATTC	1378
LaFAE1	G-CACCCCTCTCCGACACAAACTGAACA-----	1082
	* * * * *	
BnFAE1	AGGTAAGTCAGAGACTCGTGTCCAAAACGGTCCGTCTAATAAACGATGTTTGCTCTCTT	1438
LaFAE1	-----	
BnFAE1	TCGTTTCTTTTATTTGTTATAATAATTGATGGCTACGATGTTTCTCTGTTTGTTATG	1498
LaFAE1	-----	
BnFAE1	AATAAAGAAATGCAATGGTGTCTAGTATTGATTGTTTTACATGTATGTATCTCTTATT	1558
LaFAE1	-----	
BnFAE1	ACATGAAATTTTAAACGCCTAAAAAACAACGGAATTCCG	1600
LaFAE1	-----	

FIG. 7B



14/15

ALIGNMENT OF *B.n.* AND *A.t.* *FAE1* PROMOTERS CLUSTAL W (1.81) MULTIPLE SEQUENCE ALIGNMENT

```

AtFAE1 -----
BnFAE1 GGTGTTGGCAAATCTGACTTCACCAAAGAAACAACCTCGAGTCGTTATCCATCTCCTCATAA 60

AtFAE1 -----
BnFAE1 CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTTCTCTACATCGCAACCCGGC 120

AtFAE1 -----
BnFAE1 CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180

AtFAE1 -----ACTCATAAA 10
BnFAE1 GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
          *** **

AtFAE1 ACTAGTAGATTGGTTGGT--TGGTTTCCATGTACCAGAAGGCTT-----ACCCTATTAGT 63
BnFAE1 GCACGTGCGATGACTCGTCGTGSGTTGACTTCTTGAGGAAGATTCAAGAACGTCAGGTC 300
  *  **   *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 TGAAAGTTGAACTT-TGTTCCCTACT--CAATTCCTAGTTGTGTAAATGTATGTATATG 120
BnFAE1 TAGGCGATGAACTCACGGGCCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTG 360
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 TAATG-CGTATAAACGTAAGTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGAG 179
BnFAE1 CGGCGGCGCGTGAAGAGACGGAGC-AAGTTATCATTCGGTGCGCTAGAAAATCTATTCAAG 419
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 A----TGGGAGCAGAACTAAAGATGATGACATAATTAAGAACGAATTTGAAAGGCTCTTA 235
BnFAE1 AACACCAACGTTAACCCTAAAGATATAGGTATACTTGTGG-TGAACCTAAGCATGTTTAA 478
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 GGTTTGAATCCTATTTCGAGAATGTTTTTGTCAAAGATAGTGGCGA-TTTTGAACCAAAGA 294
BnFAE1 ---TCCAACCTCCATCGCTCTCCCGATGGTTCGTTAACACTTTTCAAGCTCCGAAGCAACGT 535
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 AAACATTTAAAAAATCAGTATCC--GGTTAC-GTTCATGCAA-ATAGAAAGTGGTCTAGG 350
BnFAE1 AAGAAGCTTTAACCTTGGTGGCATGGSTTGTAGTGCCSGCGTTATAGCCATTGATCTAGC 595
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ATCTGATTGTAATTTTAGACTTAAAGAGTCTCTTAAGATTCAATCCTGGCTGTGTACAAA 410
BnFAE1 AAAGGACTT--GTTGCATGTCCATAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAAC 653
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ACTACAAATAATATAT---TTTAGACTATTTGGCCTTAACTAAACTTCCACTCATTATTT 467
BnFAE1 ATCACTTATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTC 713
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ACTGAGGTTAGAGA-ATAGACTTGGGAATAAACACATTCCCGAGAAATACTCATGATCCC 526
BnFAE1 CGTGTGGTGGGGCCGCTATTTTGTCTCCAACAAG--CCTGGAGATCGTAGACGGTCCA 771
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 -----CE3-----
BnFAE1 ATAATTAGTCAGAGGGTATG--CCAATCAGATCTAAGAACACACATTCCTCTCAAATTTTA 584
  AGTACGAGCTAGTTACACGGTTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTT 831
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ATGCACATGTAATCATAGTTTAGCACAATTCAAAAATAATGTAGTATTAAAGACAGAAAT 644
BnFAE1 GCGTGCAACAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCCAAGGACATAA 891
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
  
```

FIG. 8A



15/15

ALIGNMENT OF *B.n.* AND *A.t.* *FAE1* PROMOTERS (CONTINUED)

```

AtFAE1      TTGTAGACTTTTTTTTGGCGTTAAAGGAAGACTAAG-----TTTATACGTACATTTTAT 698
BnFAE1      CCGATGTTGCTGGTTCGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTC 951
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

AtFAE1      T-TTAAGTGGAAAACCGAAATTTTCCAT-----CGAAATATATGAATTTAGTATATATA 751
BnFAE1      CGTTAAGCGAGAAACTTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATA 1011
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

                                G box 2
AtFAE1      TTTCTGCAATGTACTATTTTGGCTATTTTGGCAACTTTCAGTGGACTACTACTTTAT-TAC 810
BnFAE1      AAATCAAACATTACTACGTCCCGGATTTC-AACTTGTCTATTGACCATTTTGTATACAT 1070
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

                                G-box 1
AtFAE1      AATGTGTATGGATGCATGAGTT-TGAGTATACACATGCTCTAAATGCATGCTTTGCAAAAC 869
BnFAE1      GCCGGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGAT 1130
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

AtFAE1      GTAACGG-ACCACAAAAGAGGATCCAT-----GCAAATACATCTCATAGCTTCCTCCAT 922
BnFAE1      GTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGG 1190
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

AtFAE1      TATTTTCCGACACAAACAGA-GCA----- 945
BnFAE1      TATGAGTTGGCATACATAGAAGCAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAG 1250
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

AtFAE1      -----
BnFAE1      ATTGCTTTAGGGTCAGGCTTTAAGTGTAACAGTGCAGTTTGGGTGGCTCTAAACAATGTC 1310

AtFAE1      -----
BnFAE1      AAAGCTTCGACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATTGAT 1370

AtFAE1      -----
BnFAE1      TCTGATTCAGGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCCTAATAAACGATGTTT 1430

AtFAE1      -----
BnFAE1      GCTCTCTTTCGTTTCTTTTATTGTTATAATAATTTGATGGCTACGATGTTTCTCTGT 1490

AtFAE1      -----
BnFAE1      TTGTTATGAATAAAGAATGCAATGGTGTCTAGTATTTGATTGTTTTACATGTATGTATC 1550

AtFAE1      -----
BnFAE1      TCTTATTACATGAAATTTTTAAACGCCTAAAAAACAACGGAATTCCG 1600
    
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FIG. 8B